RHOJ GTPase cycle

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Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references


Reactome database release: 79

This document contains 1 pathway and 3 reactions (see Table of Contents)
This pathway catalogues RHOJ (also known as TCL or RHOI) guanine nucleotide exchange factors (GEFs), GTPase activator proteins (GAPs), and RHOJ effectors. No GDP dissociation inhibitors (GDIs) have been shown to interact with RHOJ. RHOJ, together with RHOQ (TC10), belongs to the CDC42 subfamily of RHO GTPases and shares 85% and 78% amino acid similarity with RHOQ and CDC42, respectively (Vignal et al. 2000). RHOJ regulates the cytoskeleton, including formation of lamellipodia and actin filaments (Vignal et al. 2000, Abe et al. 2003, Aspenstrom et al. 2004, Shi et al. 2016). RHOJ is highly expressed in endothelial cells, regulating their motility and, consequently, vascular morphogenesis (Leszczynska et al. 2011; Shi et al. 2016). As a part of the VEGF signaling cascade, RHOJ promotes retinal angiogenesis (Fukushima et al. 2013). RHOJ plays a role in cancer cell migration and cancer-related angiogenesis (Shi et al. 2016). RHOJ is involved in adipocyte differentiation (Nishizuka 2003; Shi et al. 2016).

Literature references


## Editions

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https://reactome.org
RHOJ GEFs activate RHOJ

Location: RHOJ GTPase cycle

Stable identifier: R-HSA-9017491